AMENDMENTS TO THE CLAIMS

1-11. (canceled)

12. (previously presented): A method for identifying a *Xanthomonas campestris* (*Xcc*) gene directly involved in pathogenicity, comprising:

a) introducing a broad host range cosmid comprising a transposon into a plurality of *Xcc* cells;

b) introducing an incompatible plasmid into said plurality of *Xcc* cells to drive out said broad host range cosmid comprising said transposon;

c) screening said plurality of *Xcc* cells on a selective medium to obtain an insertional *Xcc* mutant;

d) identifying a gene disrupted by said transposon in said insertional *Xcc* mutant using nucleotide amplification and sequencing;

e) inoculating said insertional *Xcc* mutant into a leaf of a host plant; and

f) assessing pathogenicity of said insertional *Xcc* mutant in said host plant,

wherein decreased pathogenicity of said insertional *Xcc* mutant, compared to a wild-type control, indicates that said disrupted gene is directly involved in *Xcc* pathogenicity.

13. (previously presented): A method for identifying a *Xanthomonas campestris* (*Xcc*) gene directly involved in pyruvate metabolism, comprising:

a) introducing a broad host range cosmid comprising a transposon into a plurality of *Xcc* cells;

b) introducing an incompatible plasmid into said plurality of *Xcc* cells to drive out said broad host range cosmid comprising said transposon;

c) screening said plurality of *Xcc* cells on a selective medium to obtain an insertional *Xcc* mutant;

d) identifying a gene disrupted by said transposon in said insertional *Xcc* mutant using nucleotide amplification and sequencing;

e) inoculating said insertional *Xcc* mutant on a solid medium comprising pyruvate as the only source of carbon; and

f) assessing growth of said insertional *Xcc* mutant on said pyruvate medium,

wherein decreased growth of said insertional *Xcc* mutant, compared to a wild-type control, indicates that said disrupted gene is directly involved in *Xcc* pyruvate metabolism.

14. (previously presented): The method of claim 12 or 13, wherein said plurality of *Xanthomonas campestris* cells comprises wild-type *Xcc* 8004 strain.

15. (previously presented): The method of claim 12 or 13, wherein said transposon is Tn5gusA5.

16. (previously presented): The method of claim 12 or 13, wherein said broad host range cosmid is pLAFR1.

17. (previously presented): The method of claim 16, wherein said incompatible plasmid is pPH1JI.

18. (previously presented): The method of claim 12 or 13, wherein said selective medium comprises kanamycin.

19. (previously presented): The method of claim 12 or 13, wherein said nucleotide amplification is performed by thermal asymmetric interlaced polymerase chain reaction (TAIL-PCR).

20. (previously presented): The method of claim 12, wherein said host plant is Chinese radish (*Raphanus sativus*), and said inoculation is performed by leaf clipping with clippers dipped in a liquid suspension of said insertional *Xcc* mutant.